

# 9

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,356A

DATE: 10/03/2001

TIME: 09:45:36

Input Set : A:\ES.txt

Output Set: N:\CRF3\10032001\I716356A.raw

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P.5

3 <110> APPLICANT: USHIO, Shimpei  
4 TORIGOE, Kakuji  
5 TANIMOTO, Tadao  
6 OKAMURA, Haruki  
7 KURIMOTO, Masashi  
8 FUKUDA, Shigeharu  
9 KUNIKATA, Toshio  
10 TANIGUCHI, Mutsuko  
11 KOHNO, Keizo  
13 <120> TITLE OF INVENTION: INTERFERON-Y INDUCING POLYPEPTIDE, PHARMACEUTICAL  
COMPOSITION THEREOF,  
14 MONOCLONAL ANTIBODY THERETO, AND METHODS OF USE  
16 <130> FILE REFERENCE: USHIO=2  
18 <140> CURRENT APPLICATION NUMBER: 09/716,356A  
19 <141> CURRENT FILING DATE: 2000-11-21  
21 <150> PRIOR APPLICATION NUMBER: 08/832,198  
22 <151> PRIOR FILING DATE: 1997-04-08  
24 <150> PRIOR APPLICATION NUMBER: 08/721,018  
25 <151> PRIOR FILING DATE: 1996-09-26  
27 <150> PRIOR APPLICATION NUMBER: 08/558,191  
28 <151> PRIOR FILING DATE: 1995-11-15  
30 <150> PRIOR APPLICATION NUMBER: 08/832,180  
31 <151> PRIOR FILING DATE: 1997-04-08  
33 <150> PRIOR APPLICATION NUMBER: 08/558,818  
34 <151> PRIOR FILING DATE: 1995-11-15  
36 <150> PRIOR APPLICATION NUMBER: 08/832,177  
37 <151> PRIOR FILING DATE: 1997-04-08  
39 <150> PRIOR APPLICATION NUMBER: 08/599,879  
40 <151> PRIOR FILING DATE: 1996-02-14  
42 <150> PRIOR APPLICATION NUMBER: 08/974,469  
43 <151> PRIOR FILING DATE: 1996-02-14  
45 <160> NUMBER OF SEQ ID NOS: 22  
47 <170> SOFTWARE: PatentIn version 3.1  
49 <210> SEQ ID NO: 1  
50 <211> LENGTH: 25  
51 <212> TYPE: PRT  
52 <213> ORGANISM: Mus sp.  
54 <400> SEQUENCE: 1  
56 Ile Ile Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile  
57 1 5 10 15  
60 Gln Ser Asp Leu Ile Phe Phe Gln Lys  
61 20 25  
64 <210> SEQ ID NO: 2  
65 <211> LENGTH: 18  
66 <212> TYPE: PRT  
67 <213> ORGANISM: Mus sp.  
69 <400> SEQUENCE: 2  
71 Gln Pro Val Phe Glu Asp Met Thr Asp Ile Asp Gln Ser Ala Ser Glu

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```

72 1          5          10          15
75 Pro Gln
79 <210> SEQ ID NO: 3
80 <211> LENGTH: 471
81 <212> TYPE: DNA
82 <213> ORGANISM: Mus sp.
84 <220> FEATURE:
85 <221> NAME/KEY: CDS
86 <222> LOCATION: (1)..(471)
87 <223> OTHER INFORMATION: Xaa is methionine or threonine
90 <400> SEQUENCE: 3
91 aac ttt ggc cga ctt cac tgt aca acc gca gta ata cgg aat ata aat      48
92 Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn
93 1          5          10          15
95 gac caa gtt ctc ttc gtt gac aaa aga cag cct gtg ttc gag gat atg      96
96 Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met
97          20          25          30
99 act gat att gat caa agt gcc agt gaa ccc cag acc aga ctg ata ata      144
100 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile
101          35          40          45
103 tac atg tac aaa gac agt gaa gta aga gga ctg gct gtg acc ctc tct      192
104 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser
105          50          55          60
107 gtg aag gat agt aaa ayg tct acc ctc tcc tgt aag aac aag atc att      240
W--> 108 Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile
109 65          70          75          80
111 tcc ttt gag gaa atg gat cca cct gaa aat att gat gat ata caa agt      288
112 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser
113          85          90          95
115 gat ctc ata ttc ttt cag aaa cgt gtt cca gga cac aac aag atg gag      336
116 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu
117          100          105          110
119 ttt gaa tct tca ctg tat gaa gga cac ttt ctt gct tgc caa aag gaa      384
120 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu
121          115          120          125
123 gat gat gct ttc aaa ctc att ctg aaa aaa aag gat gaa aat ggg gat      432
124 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
125          130          135          140
127 aaa tct gta atg ttc act ctc act aac tta cat caa agt      471
128 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
129 145          150          155
132 <210> SEQ ID NO: 4
133 <211> LENGTH: 157
134 <212> TYPE: PRT
135 <213> ORGANISM: Mus sp.
137 <220> FEATURE:
138 <221> NAME/KEY: misc_feature
139 <222> LOCATION: (70)..(70)
140 <223> OTHER INFORMATION: The 'Xaa' at location 70 stands for Thr, or Met.

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142 <400> SEQUENCE: 4
144 Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn
145 1 5 10 15
148 Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met
149 20 25 30
152 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile
153 35 40 45
156 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser
157 50 55 60
W--> 160 Val Lys Asp Ser Lys Xaa Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile
161 65 70 75 80
164 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser
165 85 90 95
168 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu
169 100 105 110
172 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu
173 115 120 125
176 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
177 130 135 140
180 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
181 145 150 155
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 471
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <220> FEATURE:
190 <221> NAME/KEY: CDS
191 <222> LOCATION: (1)..(471)
192 <223> OTHER INFORMATION: Xaa is isoleucine or threonine
195 <400> SEQUENCE: 5
196 tac ttt ggc aag ctt gaa tct aaa tta tca gtc ata aga aat ttg aat 48
197 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
198 1 5 10 15
200 gac caa gtt ctc ttc att gac caa gga aat cgg cct cta ttt gaa gat 96
201 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
202 20 25 30
204 atg act gat tct gac tgt aga gat aat gca ccc cgg acc ata ttt att 144
205 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
206 35 40 45
208 ata agt atg tat aaa gat agc cag cct aga ggt atg gct gta act atc 192
209 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
210 50 55 60
212 tct gtg aag tgt gag aaa att tca ayt ctc tcc tgt gag aac aaa att 240
W--> 213 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile
214 65 70 75 80
216 att tcc ttt aag gaa atg aat cct cct gat aac atc aag gat aca aaa 288
217 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
218 85 90 95
220 agt gac atc ata ttc ttt cag aga agt gtc cca gga cat gat aat aag 336

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221 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
222      100      105      110
224 atg caa ttt gaa tct tca tca tac gaa gga tac ttt cta gct tgt gaa      384
225 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
226      115      120      125
228 aaa gag aga gac ctt ttt aaa ctc att ttg aaa aaa gag gat gaa ttg      432
229 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
230      130      135      140
232 ggg gat aga tct ata atg ttc act gtt caa aac gaa gac      471
233 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
234 145      150      155
237 <210> SEQ ID NO: 6
238 <211> LENGTH: 157
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
242 <220> FEATURE:
243 <221> NAME/KEY: misc_feature
244 <222> LOCATION: (73)..(73)
245 <223> OTHER INFORMATION: The 'Xaa' at location 73 stands for Thr, or Ile.
247 <400> SEQUENCE: 6
249 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
250 1      5      10      15
253 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
254      20      25      30
257 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
258      35      40      45
261 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
262      50      55      60
W--> 265 Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys Glu Asn Lys Ile
266 65      70      75      80
269 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
270      85      90      95
273 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
274      100      105      110
277 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
278      115      120      125
281 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
282      130      135      140
285 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
286 145      150      155
289 <210> SEQ ID NO: 7
290 <211> LENGTH: 1120
291 <212> TYPE: DNA
292 <213> ORGANISM: Homo sapiens
294 <220> FEATURE:
295 <221> NAME/KEY: CDS
296 <222> LOCATION: (178)..(756)
297 <223> OTHER INFORMATION: Xaa is isoleucine or threonine
300 <400> SEQUENCE: 7

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301 gcctggacag tcagcaagga attgtctccc agtgcatttt gccctcctgg ctgccaactc      60
303 tggctgctaa agcggctgcc acctgctgca gtctacacag cttcggaag aggaaaggaa      120
305 ctcagacct tccagatcgc ttctctcgc aacaaactat ttgtcgcagg aataaag      177
307 atg gct gct gaa cca gta gaa gac aat tgc atc aac ttt gtg gca atg      225
308 Met Ala Ala Glu Pro Val Glu Asp Asn Cys Ile Asn Phe Val Ala Met
309 1          5          10          15
311 aaa ttt att gac aat acg ctt tac ttt ata gct gaa gat gat gaa aac      273
312 Lys Phe Ile Asp Asn Thr Leu Tyr Phe Ile Ala Glu Asp Asp Glu Asn
313          20          25          30
315 ctg gaa tca gat tac ttt ggc aag ctt gaa tct aaa tta tca gtc ata      321
316 Leu Glu Ser Asp Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile
317          35          40          45
319 aga aat ttg aat gac caa gtt ctc ttc att gac caa gga aat cgg cct      369
320 Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro
321          50          55          60
323 cta ttt gaa gat atg act gat tct gac tgt aga gat aat gca ccc cgg      417
324 Leu Phe Glu Asp Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg
325 65          70          75          80
327 acc ata ttt att ata agt atg tat aaa gat agc cag cct aga ggt atg      465
328 Thr Ile Phe Ile Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met
329          85          90          95
331 gct gta act atc tct gtg aag tgt gag aaa att tca ayt etc tcc tgt      513
W--> 332 Ala Val Thr Ile Ser Val Lys Cys Glu Lys Ile Ser Xaa Leu Ser Cys
333          100          105          110
335 gag aac aaa att att tcc ttt aag gaa atg aat cct cct gat aac atc      561
336 Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile
337          115          120          125
339 aag gat aca aaa agt gac atc ata ttc ttt cag aga agt gtc cca gga      609
340 Lys Asp Thr Lys Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly
341          130          135          140
343 cat gat aat aag atg caa ttt gaa tct tca tca tca gaa gga tac ttt      657
344 His Asp Asn Lys Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe
345 145          150          155          160
347 cta gct tgt gaa aaa gag aga gac ctt ttt aaa ctc att ttg aaa aaa      705
348 Leu Ala Cys Glu Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys
349          165          170          175
351 gag gat gaa ttg ggg gat aga tct ata atg ttc act gtt caa aac gaa      753
352 Glu Asp Glu Leu Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu
353          180          185          190
355 gac tagctattaa aatttcatgc cgggcgcagt ggctcacgcc tgtaatccca      806
356 Asp
359 gccctttggg aggetgagge gggcagatca ccagaggtca ggtgttcaag accagcctga      866
361 ccaacatggt gaaacctcat ctctactaaa aatactaaaa attagctgag tgtagtgacg      926
363 catgccctca atcccagcta ctcaagaggc tgaggcagga gaatcacttg cactccggag      986
365 gtagagggtg tggtagagcg agattgcacc attgcgtct agcctgggca acaacagcaa      1046
367 aactccatct caaaaaataa aataaataaa taaacaaata aaaaattcat aatgtgaaaa      1106
369 aaaaaaaaaa aaaa      1120
372 <210> SEQ ID NO: 8
373 <211> LENGTH: 193

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\ES.txt

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L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10